FILL Comp



Entrez

OMIMO

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix BLOSUM62 ▼ gap open: 11 gap extension: 1

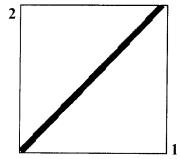
x dropoff: 30 expect: 10.000 wordsize: 3 Filter 🔽

Sequence 1 gi 829285 gluthamine synthetase [Pisum sativum]

Length 373 (1 .. 373)

Sequence 2 gi 404327 glutamate--ammonia ligase [Pinus sylvestris] Length 357 (1 .. 357)





NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 541 bits (1395), Expect = e-153Identities = 250/351 (1%), Positives = 294/351 (83%)

```
Query: 7
          DLLNLEITPFTDSIIAEYIWIGGTGIDVESHSHTISKPVSHPSEVPHWNYDGSSTGQAPG 66
           DLLNLD++ T+ +IAEYIWI GG+G+D+ESE+E++S PVS
                                                      E+PEWNYDGSSTGOA G
```

Sbjat: 7 DLLNLDLSDVTEKVIAEYIWIGGSGMDMRSKARSLSGPVSSVKELPKWNYDGSSTGQAQG 66

Sbjot: 67 HDSEVILYPÇAIFRDPFRRGKHILVICDAYSPNGTAIPSNKRAAAAKTFNEWAVSDEETW 126

YG+EQEYTLL: +VFWPLGWP+ DF++GRDI DAHYMAC+Y+GIN Sbjet: 127 YGLEQEYTLLQKDVKWPLGWPIGGYPGPÇGFYUGGVGADKAWGFDIVDAHYKACLYSGIN 186

Query: 187 ISGTNGEVMPGÇWEYQVGPSVGTEAGDHIWASKYILERITEQAGVVLTLDPFP1EGLWNG 246

ISG NGEVMPGQWE+QVGPSVG! A D ·W ·F.+I+ERITE+AGVVL+ DPMPIEGDWNG Sbjct: 187 ISGINGEVMPGQWEFQVGPSVGISAADELWCAFFIMERITEKAGVVLSFDPEPIEGDWNG 246

Query: 247 AGCHTNYSTKEMREDGGFEVIKKAILNLSLRHKIHIEAYGEGNERRLTGKHETASINDFS 306

AGCHTNYSTKSMR++GGFEVIKKAI L LRHK HI AYGEGNERRLTG+HETA +N FS Sbjot: 247 AGCHTNYSTKSMRKEGGFEVIKKAIEKLKLRHKEHISAYGEGNERRLTGRHETADMNTFS 396

Query: 307 WGVANRGOSIRWGRDTEKNGKGYLEDREPASNMDFYVVTALLAESTLLWEP 357 WGVANRG S-RYGRDTEK GKGY EDRAPASNMDPY+VT+++AE+T+LW+P

Sbjot: 307 WGVANRGASVRUGRDTEKEGKGYFEDRRPASHMDPYIVTSMIAETTILWKP 357

CPU time: 0.09 user seds. 0.02 sys. seds 0.11 total seds.

```
K H
0.136 0.416
Lambda
   0.315
Japped.
Lambda
           0.0410 0.140
  0.267
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 1090
Number of Sequences: 0
Number if extensions: 73
Number of successful extensions: 2
Number if sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of ESP's gapped (non-prelim): 1
length of query: 373
length of database: 445,599,717
affective HSP length: 128
effective length of query: 245
effective length of database: 445,599,589
effective search space: 109171899305
effective search space used: 109171899305
T: 9
A: 4()
M1: 16 + 7.3 bits: M2: 77 29.7 bits
X3: 77 (29.7 bits)
S1: 42 (22.0 bits)
S2: 75 (33.5 bits)
```



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BLAST

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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.5 [Nov-16-2002]

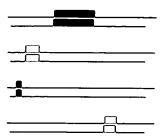
Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

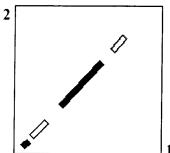
x dropoff: 50 expect: 10.00€ wordsize: 11 Filter ✓ Align

Sequence 1 gi 404326 P.sylvestris mRNA for glutamine synthetase

Length 1423 (1 .. 1423)

Sequence 2 gi 20752 Pea leaf mRNA for glutamine synthetase (EC 6.3.1.2) Length 1304 (1 .. 1304)





NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 160 bits (93), Expect = 66-36Identities = 285/386 (73*) Strand = Plus / Plus

Query: $454\ \ \text{aaatggcctcttggctggccaattggtggctaccccggtcctcagggcccatattact}$ tributer of the common about the state of th Sbict: 423 aaatggccattaggttggcctgtaggtggctatcccggtcctcagggtccttattact gluthamine synthetase 141 K W P L G W P V G G Y P G P Q G P Y Y Query: 514 ggagttggagetgaeaaageetggggaegagaeattgttgatgeeeaftataaggett Sbict: $483\ {\tt gctgccggagcagataagtcatttggacgtgatatatctgatgctcattacaaggctt}$ gluthamine synthetase 161 A A G A D K S F G R D I S D A H Y K A Query: 574 ototattoaggaatoaatatoagtggcatbaatggagaagtcatgobagggbagtggg of the the beautiful and the contribution Sbict: 543 atatatgotggaáttaacattagtggsacsaatggagaagttatgcotggacagtggg gluthamine synthetase 181 I Y A G I N I S G T N G E V M P G Q W Query: 634 tittoaagtaggtoogtoagtgggtateleagoagoagatgagorgrygtgotogtt

```
Sbfat:
                  803 tatomaguiygtoolagigtaggtatigaaguiggigatoatatoigggottoaoggt
gluthamine synthetase 201 Y . V G F S V G I E A G D H I W A S R
Query:
                  694 attatggagaggattacagaaaaggoyggtgtogttutgtootttgatuccaagccaa
                     663 attottigagagaattad gaadaagotygtgtigtgdtcadtottgatddaaaaddaa
Sbjat:
gluthamine synthetase 221 I L E R I T E Q A G 7 V L T L D P K P
Query:
                  T54 gagggggactggaatggtgctggatgccacacacaaattacagcaccaagtccatgcgca
                      Sbjct:
                  723 gagggtgattggaatggtgcaggatgtcacaccaattacagtacaaagagcatgaggg
gluthamine synthetase 241 E G D W N G A G C H T N Y S T K S M R
Query:
                  814 gagggaggcttcgaagtaattaagaa 839
                     Sbict:
                  783 gatggagggtttgaggtgataaagaa 808
gluthamine synthetase 261 D G G F E V I K K
Score = 68.0 bits (35), Expect = 4e+08
Identities = 103/137 (75)
 Strand = Plus / Plus
Query:
                  181 gagetteceaaatggaactatgaeggetecageactggaeaggeteaaggaeatgaea
                     Sbjct:
                  150 \ gaggttcctaagtggaactatgatggatctagcactggacaagcccstggtgaagata
gluthamine synthetase 50 E V P K W N Y D G S S T G Q A P G E D
Query:
                  241 gaagteattetatateeacaagetatetteegtgateeatttegeagaggaaageaca
                     Sb-ct:
                  210 gaagtgateetatateeteaagcaatttteaaagateettteegtggeggaaacaata
gluthamine synthetase 70 \, E \, V \, I \, L \, Y \, P \, Q \, A \, I \, F \, K \, D \, P \, F \, R \, G \, G \, N \, N
Query:
                  301 ttggtaatctgtgatgs 317
                     Sbict:
                  270 ttggtcgtttgtgatgc 286
gluthamine synthetase 90 L V V C D A
Score = 52.6 \text{ bits } (27), Expect = 0.002
Identities = 43/51 (84.)
 Strand - Plus / Plus
Query:
                  94 attgcagagtatatatggattggaggatbaggaatggatatgcgcagtaaa 144
                     todas (botto) il minutati di salumni sali filitori della
Sbict:
                     attgctgagtacatatggattggtgggacaggaattyatgtqcgcagcaaa 113
Score = 46.8 bits (24), Except = 0.089
Identities = 84/114 (73)
Strand = Plus / Flus
```

```
945 cttttsstggggtgttgcaaatcgaggagettsagttagagtgggssgggasacaga
Query:
                          alled HUII to be at the fit and a compact of the fit
Sbrat:
                     914
                          \verb|cttttcttggggagtggctaaccggggatgctcaatccgtgtgggaagagacaccga|\\
aluthamine synthetase 305
                          F S W G V A N R G C S I R V G R D T E
luery:
                     1005 agaaggaaaaggttattttgaggaccgtcgacctgcttcaaacatggatccata 10
                           3bist:
                     974
                          gaatggcaaaggttacttggaagacaggcgtccggcttcgaacatggatccata 10
gluthamine synthetase 325
                          N 3 K G Y L E D R R P A S N M D P Y
CPU time:
            0.03 user secs.
                                 0.07 sys. secs
                                                         0.15 total secs.
Lambda
          F.
           0.521
   1.3
Bapped
Lambida
   1.37
          0.621
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6
Number of Sequences: 0
Number of extensions: 6
Number fs.coesaful extensions: 5
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 4
length of query: 1423
length of database: 7,976,531,563
effective H3P length: 25
effective length of query: 1398
effective length of database: 7,976,831,538
effective search space: 11151191090124
effective search space used: 11151191090124
T: 0
A: 0
X1: ₹ (11.5 bits)
X2: 26 50.0 bits:
$1: 12 23.8 bits:
$2: 21 (41.1 bits)
```